

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/550,5/8  
Source: Pr/10  
Date Processed by STIC: 10/5/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 10/05/2005

PATENT APPLICATION: US/10/550,518

TIME: 16:22:40

Input Set : A:\sequence listing ascii.txt

Output Set: N:\CRF4\10052005\J550518.raw

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3 <110> APPLICANT: Cytos Biotechnology AG
4     Maurer, Patrik
5     Bachmann, Martin
6     Proba, Karl
7     Meijerink, Edwin
8     Manolova, Vania
10 <120> TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like
11     Particles: Method of Preparation and Use
13 <130> FILE REFERENCE: 1700.0630000
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/550,518
C--> 15 <141> CURRENT FILING DATE: 2005-09-23
15 <150> PRIOR APPLICATION NUMBER: 60/457,348
16 <151> PRIOR FILING DATE: 2003-03-26
18 <160> NUMBER OF SEQ ID NOS: 111
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 10
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: oligonucleotide ISS
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35 <211> LENGTH: 19
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: oligonucleotide G3-6
42 <400> SEQUENCE: 2
43 ggggacgatc gtcggggggg                         19
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47 <211> LENGTH: 20
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: oligonucleotide G4-6
54 <400> SEQUENCE: 3
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58 <210> SEQ ID NO: 4
59 <211> LENGTH: 21
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial sequence

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63 <220> FEATURE:
64 <223> OTHER INFORMATION: oligonucleotide G5-6
66 <400> SEQUENCE: 4
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70 <210> SEQ ID NO: 5
71 <211> LENGTH: 22
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: oligonucleotide G6-6
78 <400> SEQUENCE: 5
79 gggggggacg atcgtcgggg gg 22
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 24
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: oligonucleotide G7-7
90 <400> SEQUENCE: 6
91 ggggggggac gatcgtcggg gggg 24
94 <210> SEQ ID NO: 7
95 <211> LENGTH: 26
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: oligonucleotide G8-8
102 <400> SEQUENCE: 7
103 gggggggggga cgatcgtcgg gggggg 26
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 28
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: oligonucleotide G9-9
114 <400> SEQUENCE: 8
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118 <210> SEQ ID NO: 9
119 <211> LENGTH: 30
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: oligonucleotide G6
126 <400> SEQUENCE: 9
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130 <210> SEQ ID NO: 10
131 <211> LENGTH: 132
132 <212> TYPE: PRT
133 <213> ORGANISM: Bacteriophage Q-beta
135 <400> SEQUENCE: 10

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137 Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
138 1 5 10 15
141 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
142 20 25 30
145 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
146 35 40 45
149 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
150 50 55 60
153 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
154 65 70 75 80
157 Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
158 85 90 95
161 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
162 100 105 110
165 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
166 115 120 125
169 Asn Pro Ala Tyr
170 130
173 <210> SEQ ID NO: 11
174 <211> LENGTH: 328
175 <212> TYPE: PRT
176 <213> ORGANISM: Bacteriophage Q-beta
178 <400> SEQUENCE: 11
180 Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
181 1 5 10 15
184 Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
185 20 25 30
188 Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
189 35 40 45
192 Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
193 50 55 60
196 Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
197 65 70 75 80
200 Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
201 85 90 95
204 Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
205 100 105 110
208 Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
209 115 120 125
212 Leu Asn Pro Ala Tyr Trp Leu Leu Ile Ala Gly Gly Gly Ser Gly Ser
213 130 135 140
216 Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro Gly
217 145 150 155 160
220 Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu Val
221 165 170 175
224 Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala Val
225 180 185 190
228 Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu Gly
229 195 200 205

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232 Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr Phe
233      210                      215                      220
236 Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr Leu
237 225                      230                      235                      240
240 Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu Gly
241                      245                      250                      255
244 Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu Lys
245                      260                      265                      270
248 Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His Ala
249                      275                      280                      285
252 Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly Ala
253      290                      295                      300
256 Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile Gln
257 305                      310                      315                      320
260 Ala Val Ile Val Val Pro Arg Ala
261                      325
264 <210> SEQ ID NO: 12
265 <211> LENGTH: 362
266 <212> TYPE: PRT
267 <213> ORGANISM: BK virus
269 <400> SEQUENCE: 12
271 Met Ala Pro Thr Lys Arg Lys Gly Glu Cys Pro Gly Ala Ala Pro Lys
272 1                      5                      10                      15
275 Lys Pro Lys Glu Pro Val Gln Val Pro Lys Leu Leu Ile Lys Gly Gly
276      20                      25                      30
279 Val Glu Val Leu Glu Val Lys Thr Gly Val Asp Ala Ile Thr Glu Val
280      35                      40                      45
283 Glu Cys Phe Leu Asn Pro Glu Met Gly Asp Pro Asp Asp Asn Leu Arg
284      50                      55                      60
287 Gly Tyr Ser Gln His Leu Ser Ala Glu Asn Ala Phe Glu Ser Asp Ser
288 65                      70                      75                      80
291 Pro Asp Arg Lys Met Leu Pro Cys Tyr Ser Thr Ala Arg Ile Pro Leu
292      85                      90                      95
295 Pro Asn Leu Asn Glu Asp Leu Thr Cys Gly Asn Leu Leu Met Trp Glu
296      100                     105                     110
299 Ala Val Thr Val Lys Thr Glu Val Ile Gly Ile Thr Ser Met Leu Asn
300      115                     120                     125
303 Leu His Ala Gly Ser Gln Lys Val His Glu Asn Gly Gly Gly Lys Pro
304      130                     135                     140
307 Val Gln Gly Ser Asn Phe His Phe Phe Ala Val Gly Gly Asp Pro Leu
308 145                     150                     155                     160
311 Glu Met Gln Gly Val Leu Met Asn Tyr Arg Thr Lys Tyr Pro Gln Gly
312      165                     170                     175
315 Thr Ile Thr Pro Lys Asn Pro Thr Ala Gln Ser Gln Val Met Asn Thr
316      180                     185                     190
319 Asp His Lys Ala Tyr Leu Asp Lys Asn Asn Ala Tyr Pro Val Glu Cys
320      195                     200                     205
323 Trp Ile Pro Asp Pro Ser Arg Asn Glu Asn Thr Arg Tyr Phe Gly Thr
324      210                     215                     220

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327 Tyr Thr Gly Gly Glu Asn Val Pro Pro Val Leu His Val Thr Asn Thr
328 225                230                235                240
331 Ala Thr Thr Val Leu Leu Asp Glu Gln Gly Val Gly Pro Leu Cys Lys
332                245                250                255
335 Ala Asp Ser Leu Tyr Val Ser Ala Ala Asp Ile Cys Gly Leu Phe Thr
336                260                265                270
339 Asn Ser Ser Gly Thr Gln Gln Trp Arg Gly Leu Ala Arg Tyr Phe Lys
340                275                280                285
343 Ile Arg Leu Arg Lys Arg Ser Val Lys Asn Pro Tyr Pro Ile Ser Phe
344                290                295                300
347 Leu Leu Ser Asp Leu Ile Asn Arg Arg Thr Gln Lys Val Asp Gly Gln
348 305                310                315                320
351 Pro Met Tyr Gly Met Glu Ser Gln Val Glu Glu Val Arg Val Phe Asp
352                325                330                335
355 Gly Thr Glu Gln Leu Pro Gly Asp Pro Asp Met Ile Arg Tyr Ile Asp
356                340                345                350
359 Arg Gln Gly Gln Leu Gln Thr Lys Met Val
360                355                360
363 <210> SEQ ID NO: 13
364 <211> LENGTH: 130
365 <212> TYPE: PRT
366 <213> ORGANISM: Bacteriophage fr
368 <400> SEQUENCE: 13
370 Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
371 1                5                10                15
374 Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
375                20                25                30
378 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
379                35                40                45
382 Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
383                50                55                60
386 Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
387 65                70                75                80
390 Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
391                85                90                95
394 Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
395                100                105                110
398 Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
399                115                120                125
402 Ile Tyr
403                130
406 <210> SEQ ID NO: 14
407 <211> LENGTH: 130
408 <212> TYPE: PRT
409 <213> ORGANISM: Bacteriophage GA
411 <400> SEQUENCE: 14
413 Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
414 1                5                10                15
417 Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp

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**VERIFICATION SUMMARY**

DATE: 10/05/2005

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TIME: 16:22:41

Input Set : A:\sequence listing ascii.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date